

SEQUENCE LISTING

<110> Majumder, Arunendra
Manoj, Majee

<120> A salt tolerant L-myo-inositol 1-phosphate synthase and the process of obtaining the same

<130> 4544-051674

<140> US 10/538,423

<141> 2005-06-10

<150> PCT/IN2003/000065

<151> 2003-03-21

<160> 3

<170> MicrosoftWord 2003

<210> 1

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<212> DNA

<213> Porteresia coarctata

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<213> *Oryza sativa*

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<400> 2

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His	Glu	Ser	His	Asp	Gly	Ala	Ser	Arg	Tyr	Ile	Val	Arg	Pro	Lys	Ser	35	40	45	
Val	Arg	Tyr	Asn	Phe	Arg	Thr	Thr	Thr	Thr	Val	Pro	Lys	Leu	Gly	Val	50	55	60	
Met	Leu	Val	Gly	Tyr	Gly	Gly	Asn	Asn	Gly	Ser	Thr	Leu	Thr	Ala	Gly	65	70	75	80
Val	Ile	Ala	Asp	Arg	Glu	Gly	Ile	Ser	Trp	Ala	Thr	Lys	Asp	Lys	Val	85	90	95	
Gln	Gln	Ala	Asn	Tyr	Tyr	Gly	Ser	Leu	Thr	Gln	Ala	Ser	Thr	Ile	Arg	100	105	110	
Val	Gly	Ser	Tyr	Asn	Gly	Glu	Glu	Ile	Tyr	Ala	Pro	Phe	Lys	Ser	Leu	115	120	125	
Leu	Pro	Met	Val	Asn	Pro	Asp	Asp	Leu	Val	Phe	Gly	Gly	Trp	Asp	Ile	130	135	140	

Ser	Asn	Met	Asn	Leu	Ala	Asp	Ala	Met	Thr	Arg	Ala	Lys	Val	Leu	Asp	
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Ile	Asp	Leu	Gln	Lys	Gln	Leu	Arg	Pro	Tyr	Met	Glu	Ser	Met	Val	Pro	
				165					170					175		
Leu	Pro	Gly	Ile	Tyr	Asp	Pro	Asp	Val	Ile	Ala	Ala	Asn	Gln	Gly	Ser	
			180					185					190			
Arg	Ala	Asn	Asn	Val	Ile	Lys	Gly	Thr	Lys	Lys	Glu	Gln	Met	Glu	Gln	
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Ile	Ile	Lys	Asp	Ile	Arg	Glu	Phe	Lys	Glu	Lys	Ser	Lys	Val	Asp	Lys	
	210					215					220					
Val	Val	Val	Leu	Trp	Thr	Ala	Asn	Thr	Glu	Arg	Tyr	Ser	Asn	Val	Cys	
225					230					235					240	
Val	Gly	Leu	Asn	Asp	Thr	Met	Glu	Asn	Leu	Leu	Ala	Ser	Val	Asp	Lys	
				245					250					255		
Asn	Glu	Ala	Glu	Ile	Ser	Pro	Ser	Thr	Leu	Tyr	Ala	Ile	Ala	Cys	Val	
			260					265					270			
Met	Glu	Gly	Ile	Pro	Phe	Ile	Asn	Gly	Ser	Pro	Gln	Asn	Thr	Phe	Val	
		275					280					285				
Pro	Gly	Leu	Ile	Asp	Leu	Ala	Ile	Lys	Asn	Asn	Cys	Leu	Ile	Gly	Gly	
	290					295					300					
Asp	Asp	Phe	Lys	Ser	Gly	Gln	Thr	Lys	Met	Lys	Ser	Val	Leu	Val	Asp	
305					310					315					320	
Phe	Leu	Val	Gly	Ala	Gly	Ile	Lys	Pro	Thr	Ser	Ile	Val	Ser	Tyr	Asn	
				325					330					335		
His	Leu	Gly	Asn	Asn	Asp	Gly	Met	Asn	Leu	Ser	Ala	Pro	Gln	Thr	Phe	
			340					345					350			
Arg	Ser	Lys	Glu	Ile	Ser	Lys	Ser	Asn	Val	Val	Asp	Asp	Met	Val	Ser	
		355					360					365				
Ser	Asn	Ala	Ile	Leu	Tyr	Glu	Leu	Gly	Glu	His	Pro	Asp	His	Val	Val	
			370			375					380					
Val	Ile	Lys	Tyr	Val	Pro	Tyr	Val	Gly	Asp	Ser	Lys	Arg	Ala	Met	Asp	
385					390					395					400	
Glu	Tyr	Thr	Ser	Glu	Ile	Phe	Met	Gly	Gly	Lys	Ser	Thr	Ile	Val	Leu	
				405					410					415		
His	Asn	Thr	Cys	Glu	Asp	Ser	Leu	Leu	Ala	Ala	Pro	Ile	Ile	Leu	Asp	
			420					425					430			
Leu	Val	Leu	Leu	Ala	Glu	Leu	Ser	Thr	Arg	Ile	Gln	Leu	Lys	Ala	Glu	
		435					440					445				

Gly Glu Glu Lys Phe His Ser Phe His Pro Val Ala Thr Ile Leu Ser
 450 455 460

Tyr Leu Thr Lys Ala Pro Leu Val Pro Pro Gly Thr Pro Val Val Asn
 465 470 475 480

Ala Leu Ala Lys Gln Arg Ala Met Leu Glu Asn Ile Met Arg Ala Cys
 485 490 495

Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
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<210> 3

<211> 512

<212> PRT

<213> *Porteresia coarctata*

<220>

<400> 3

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His Glu Ser His Asp Gly Ala Ser Arg Tyr Val Val Arg Pro Lys Ser
 35 40 45

Val Gln Tyr His Phe Arg Thr Ser Thr Thr Val Pro Lys Leu Gly Val
 50 55 60

Met Leu Val Gly Tyr Gly Gly Asn Asn Gly Ser Thr Leu Thr Ala Gly
 65 70 75 80

Val Ile Ala Ser Arg Glu Gly Ile Ser Trp Ala Thr Lys Asp Lys Val
 85 90 95

Gln Gln Ala Asn Tyr Tyr Gly Ser Leu Thr Gln Ala Ser Thr Ile Arg
 100 105 110

Val Gly Ser Tyr Asn Gly Glu Glu Ile Tyr Ala Pro Phe Lys Ser Leu
 115 120 125

Leu Pro Met Val Asn Pro Asp Asp Leu Val Phe Gly Gly Trp Asp Ile
 130 135 140

Ser Asn Met Asn Leu Ala Asp Ala Met Thr Arg Ala Lys Val Leu Asp
 145 150 155 160

Ile Asp Leu Gln Lys Gln Leu Arg Pro Tyr Met Glu Ser Trp Cys Leu
 165 170 175

Ser Leu Ala Ser Met Ile Pro Thr Ser Ser Pro Leu Thr Arg Asp Pro
 180 185 190

Ala	Arg	Thr	Met	Ser	Ser	Arg	Glu	Pro	Arg	Arg	Ser	Arg	Trp	Gly	Arg	195	200	205
Ser	Ser	Lys	Asp	Ile	Arg	Glu	Phe	Lys	Glu	Asn	Asn	Lys	Met	Asp	Lys	210	215	220
Ala	Val	Val	Leu	Trp	Thr	Ala	Asn	Thr	Glu	Arg	Tyr	Asn	Asn	Cys	Leu	225	230	235
Cys	Leu	Gly	Leu	Met	Thr	Asn	Gly	Lys	Pro	Ser	Ala	Ser	Val	Asp	Arg	245	250	255
Asn	Gln	Ala	Glu	Ile	Ser	Pro	Ser	Thr	Leu	Tyr	Cys	His	Cys	Leu	Ala	260	265	270
Ser	Leu	Glu	Gly	Val	Arg	Ser	Ile	Thr	Gly	Ala	Leu	Lys	Lys	Lys	Ser	275	280	285
Trp	Pro	Gly	Ile	Asp	Asp	Leu	Ala	Ile	Lys	Lys	Lys	Leu	Pro	Asp	Pro	290	295	300
Gly	Gly	Leu	Ile	Gln	Lys	Arg	Gly	Lys	Pro	Lys	Lys	Lys	Thr	Gly	Leu	305	310	315
Val	Asp	Phe	Leu	Met	Gly	Ala	Gly	Ile	Lys	Pro	Thr	Ser	Ile	Val	Ser	325	330	335
Tyr	Asn	His	Leu	Gly	Asn	Asn	Asp	Gly	Met	Asn	Leu	Ser	Ala	Pro	Gln	340	345	350
Thr	Phe	Arg	Ser	Lys	Glu	Ile	Ser	Lys	Ser	Ser	Val	Val	Asp	Asp	Met	355	360	365
Val	Ser	Ser	Asn	Ala	Ile	Leu	Tyr	Glu	Leu	Gly	Glu	His	Pro	Asp	His	370	375	380
Val	Val	Val	Ile	Lys	Tyr	Val	Pro	Tyr	Val	Gly	Asp	Ser	Lys	Arg	Ala	385	390	395
Met	Asp	Glu	Tyr	Thr	Ser	Glu	Ile	Phe	Met	Gly	Gly	Lys	Asn	Thr	Ile	405	410	415
Val	Leu	His	Asn	Thr	Cys	Glu	Asp	Ser	Leu	Leu	Ala	Ala	Pro	Ile	Ile	420	425	430
Leu	Asp	Leu	Val	Leu	Leu	Ala	Glu	Leu	Ser	Thr	Arg	Ile	Gln	Leu	Lys	435	440	445
Gly	Glu	Gly	Glu	Glu	Lys	Phe	His	Ser	Phe	His	Pro	Val	Ala	Thr	Ile	450	455	460
Leu	Ser	Tyr	Leu	Thr	Lys	Ala	Pro	Leu	Val	Pro	Pro	Gly	Thr	Pro	Val	465	470	475
Val	Asn	Ala	Leu	Ala	Lys	Gln	Arg	Ala	Met	Leu	Glu	Asn	Ile	Met	Arg	485	490	495

Ala Cys Val Gly Leu Ala Pro Glu Asn Asn Met Ile Leu Glu Tyr Lys
500 505 510